

#13
P3
3/17/02

RAW SEQUENCE LISTING DATE: 07/17/2002
 PATENT APPLICATION: US/09/315,116 TIME: 13:52:34

Input Set : N:\Crif3\RULE60\09315116.raw
 Output Set: N:\CRF3\07172002\I315116.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Antelman, Douglas
 6 Gregory, Richard J.
 7 Wils, Kenneth N.
 9 (ii) TITLE OF INVENTION: Tissue Specific Expression of
 10 Retinoblastoma Protein

12 (iii) NUMBER OF SEQUENCES: 46

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
 16 (B) STREET: Two Embarcadero Center, 8th Floor
 17 (C) CITY: San Francisco
 18 (D) STATE: CA
 19 (E) COUNTRY: USA
 20 (F) ZIP: 94111

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk
 24 (B) COMPUTER: IBM PC compatible
 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/315,116
 C--> 30 (B) FILING DATE: 19-May-1999
 40 (C) CLASSIFICATION: 514

33 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: US/08/801,092
 36 (B) FILING DATE: 14-FEB-1997
 38 (A) APPLICATION NUMBER: US 08/751,517
 39 (B) FILING DATE: 15-NOV-1996

42 (viii) ATTORNEY/AGENT INFORMATION:

43 (A) NAME: Fitts, Renee A.
 44 (B) REGISTRATION NUMBER: 35,136
 45 (C) REFERENCE/DOCKET NUMBER: 016930-001020

47 (ix) TELECOMMUNICATION INFORMATION:

48 (A) TELEPHONE: 415-576-0200
 49 (B) TELEFAX: 703-576-0300

52 (2) INFORMATION FOR SEQ ID NO: 1:

54 (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 437 amino acids
 56 (B) TYPE: amino acid
 57 (C) STRANDEDNESS: Not Relevant
 W--> 58 (D) TOPOLOGY: Not Relevant

60 (ii) MOLECULE TYPE: peptide

ENTERED

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65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
67 Met Ala Leu Ala Gly Ala Pro Ala Gly Gly Pro Cys Ala Pro Ala Leu
68 1 5 10 15
70 Glu Ala Leu Leu Gly Ala Gly Ala Leu Arg Leu Leu Asp Ser Ser Gln
71 20 25 30
73 Ile Val Ile Ile Ser Ala Ala Gln Asp Ala Ser Ala Pro Ala Pro
74 35 40 45
76 Thr Gly Pro Ala Ala Pro Ala Ala Gly Pro Cys Asp Pro Asp Leu Leu
77 50 55 60
79 Leu Phe Ala Thr Pro Gln Ala Pro Arg Pro Thr Pro Ser Ala Pro Arg
80 65 70 75 80
82 Pro Ala Leu Gly Arg Pro Pro Val Lys Arg Arg Leu Asp Leu Glu Thr
83 85 90 95
85 Asp His Gln Tyr Leu Ala Glu Ser Ser Gly Pro Ala Arg Gly Arg Gly
86 100 105 110
88 Arg His Pro Gly Lys Gly Val Lys Ser Pro Gly Glu Lys Ser Arg Tyr
89 115 120 125
91 Glu Thr Ser Leu Asn Leu Thr Thr Lys Arg Phe Leu Glu Leu Leu Ser
92 130 135 140
94 His Ser Ala Asp Gly Val Val Asp Leu Asn Trp Ala Ala Glu Val Leu
95 145 150 155 160
97 Lys Val Gln Lys Arg Arg Ile Tyr Asp Ile Thr Asn Val Leu Glu Gly
98 165 170 175
100 Ile Gln Leu Ile Ala Lys Lys Ser Lys Asn His Ile Gln Trp Leu Gly
101 180 185 190
103 Ser His Thr Thr Val Gly Val Gly Gly Arg Leu Glu Gly Leu Thr Gln
104 195 200 205
106 Asp Leu Arg Gln Leu Gln Glu Ser Glu Gln Gln Leu Asp His Leu Met
107 210 215 220
109 Asn Ile Cys Thr Thr Gln Leu Arg Leu Leu Ser Glu Asp Thr Asp Ser
110 225 230 235 240
112 Gln Arg Leu Ala Tyr Val Thr Cys Gln Asp Leu Arg Ser Ile Ala Asp
113 245 250 255
115 Pro Ala Glu Gln Met Val Met Val Ile Lys Ala Pro Pro Glu Thr Gln
116 260 265 270
118 Leu Gln Ala Val Asp Ser Ser Glu Asn Phe Gln Ile Ser Leu Lys Ser
119 275 280 285
121 Lys Gln Gly Pro Ile Asp Val Phe Leu Cys Pro Glu Glu Thr Val Gly
122 290 295 300
124 Gly Ile Ser Pro Gly Lys Thr Pro Ser Gln Glu Val Thr Ser Glu Glu
125 305 310 315 320
127 Glu Asn Arg Ala Thr Asp Ser Ala Thr Ile Val Ser Pro Pro Pro Ser
128 325 330 335
130 Ser Pro Pro Ser Ser Leu Thr Thr Asp Pro Ser Gln Ser Leu Leu Ser
131 340 345 350
133 Leu Glu Gln Glu Pro Leu Leu Ser Arg Met Gly Ser Leu Arg Ala Pro
134 355 360 365
136 Val Asp Glu Asp Arg Leu Ser Pro Leu Val Ala Ala Asp Ser Leu Leu
137 370 375 380

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139      Glu His Val Arg Glu Asp Phe Ser Gly Leu Leu Pro Glu Glu Phe Ile
140      385                      390                      395                      400
142      Ser Leu Ser Pro Pro His Glu Ala Leu Asp Tyr His Phe Gly Leu Glu
143                      405                      410                      415
145      Glu Gly Glu Gly Ile Arg Asp Leu Phe Asp Cys Asp Phe Gly Asp Leu
146                      420                      425                      430
148      Thr Pro Leu Asp Phe
149                      435

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151 (2) INFORMATION FOR SEQ ID NO: 2:

153 (i) SEQUENCE CHARACTERISTICS:

154 (A) LENGTH: 2517 base pairs

155 (B) TYPE: nucleic acid

156 (C) STRANDEDNESS: single

157 (D) TOPOLOGY: linear

163 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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165 GGAATTCCGT GGCCGGGACT TTGCAGGCAG CGGCGGCCGG GGGCGGAGCG GGATCGAGCC      60
167 CTCGCCGAGG CCTGCCGCCA TGGGCCCGCG CCGCCGCCGC CGCCTGTAC CC GGCGCCGCG      120
169 CGGGCCGTGA GCGTCATGGC CTTGGCCGGG GCCCTGCGG GCGGCCCATG CGCGCCGCGCG      180
171 CTGGAGGCCC TGCTCGGGGC CGGCGCGCTG CGGCTGCTCG ACTCCTCGCA GATCGTCATC      240
173 ATCTCCGCCG CGCAGGACGC CAGCGCCCCG CCGGCTCCCA CCGGCCCCGC GCGCCCCGCC      300
175 GCCGGCCCCCT GCGACCCTGA CCTGCTGTCTC TTCGCCACAC CGCAGGCGCC CCGGCCACAC      360
177 CCCAGTGCGC CGCGGCCCGC GCTCGGCCGC CCGCCGGTGA AGCGGAGGCT GGACCTGGAA      420
179 ACTGACCATC AGTACCTGGC CGAGAGCAGT GGGCCAGCTC GGGGCAGAGG CCGCCATCCA      480
181 GGAAAAGGTG TGAATCCCC GGGGGAGAAG TCACGCTATG AGACCTCACT GAATCTGACC      540
183 ACCAAGCGCT TCCTGGAGCT GCTGAGCCAC TCGGCTGACG GTGTCGTCGA CCTGAACTGG      600
185 GCTGCCGAGG TGCTGAAGGT GCAGAAGCGG CGCATCTATG ACATCACCAA CGTCCCTTGAG      660
187 GGCATCCAGC TCATTGCCAA GAAGTCCAAG AACCACATCC AGTGGCTGGG CAGCCACACC      720
189 ACAGTGGGCG TCGGCGGACG GCTTGAGGGG TTGACCCAGG ACCTCCGACA GCTGCAGGAG      780
191 AGCGAGCAGC AGCTGGACCA CCTGATGAAT ATCTGTACTA CGCAGCTGCG CCTGCTCTCC      840
193 GAGGACACTG ACAGCCAGCG CCTGGCCTAC GTGACGTGTC AGGACCTTCG TAGCATTGCA      900
195 GACCCTGCAG AGCAGATGGT TATGGTGATC AAAGCCCCTC CTGAGACCCA GCTCCAAGCC      960
197 GTGGACTCTT CGGAGAACTT TCAGATCTCC CTTAAGAGCA AACAAGGCCC GATCGATGTT      1020
199 TTCCTGTGCC CTGAGGAGAC CGTAGGTGGG ATCAGCCCTG GGAAGACCCC ATCCCAGGAG      1080
201 GTCACTTCTG AGGAGGAGAA CAGGGCCACT GACTCTGCCA CCATAGTGTC ACCACCACCA      1140
203 TCATCTCCCC CCTCATCCCT CACCACAGAT CCCAGCCAGT CTCTACTCAG CCTGGAGCAA      1200
205 GAACCGCTGT TGTCCCGGAT GGGCAGCCTG CGGGCTCCCG TGGACGAGGA CCGCCTGTCC      1260
207 CCGCTGGTGG CGGCCGACTC GCTCCTGGAG CATGTGCGGG AGGACTTCTC CGGCCTCCTC      1320
209 CCTGAGGAGT TCATCAGCCT TTCCCCACCC CACGAGGCCC TCGACTACCA CTTGCGCCTC      1380
211 GAGGAGGGCG AGGGCATCAG AGACCTCTTC GACTGTGACT TTGGGGACCT CACCCCCCTG      1440
213 GATTCTGAC AGGGCTTGA GGGACCAGG TTTCCAGAGT AGCTCACCTT GTCTCTGCAG      1500
215 CCCTGGAGCC CCCTGTCCCT GGCCGTCCCT CCAGCCTGTT TGGAAACATT TAATTTATAC      1560
217 CCCTCTCCTC TGTCTCCAGA AGCTTCTAGC TCTGGGGTCT GGCTACCGCT AGGAGGCTGA      1620
219 GCAAGCCAGG AAGGGAAGGA GTCTGTGTGG TGTGTATGTG CATGCAGCCT ACACCCACAC      1680
221 GTGTGTACCG GGGGTGAATG TGTGTGAGCA TGTGTGTGTG CATGTACCGG GGAATGAAGG      1740
223 TGAACATACA CCTCTGTGTG TGCACTGCAG ACACGCCCCA GTGTGTCCAC ATGTGTGTGC      1800
225 ATGAGTCCAT CTCTGCGCGT GGGGGGGCTC TAACTGCACT TTCGGCCCTT TTGCTCGTGG      1860
227 GGTCCCACAA GGCCAGGGC AGTGCCTGCT CCCAGAATCT GGTGCTCTGA CCAGGCCAGG      1920
229 TGGGGAGGCT TTGGCTGGCT GGGCGTGTAG GACGCTGAGA GCACTTCTGT CTTAAAGGTT      1980
231 TTTTCTGATT GAAGCTTTAA TGGAGCGTTA TTTATTTATC GAGGCCTCTT TGGTGAGCCT      2040

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233 GGGGAATCAG CAAAAGGGGA GGAGGGGTGT GGGGTTGATA CCCCAACTCC CTCTACCCCTT 2100
235 GAGCAAGGGC AGGGGTCCCT GAGCTGTTCT TCTGCCCCAT ACTGAAGGAA CTGAGGCCTG 2160
237 GGTGATTTAT TTATTGGGAA AGTGAGGGAG GGAGACAGAC TGACTGACAG CCATGGGTGG 2220
239 TCAGATGGTG GGGTGGGCCC TCTCCAGGGG GCCAGTTCAG GGCCAGCTG CCCCCAGGA 2280
241 TGGATATGAG ATGGGAGAGG TGAGTGGGGG ACCTTCACTG ATGTGGGCAG GAGGGGTGGT 2340
243 GAAGGCCTCC CCCAGCCCAG ACCCTGTGGT CCCTCCTGCA GTGTCTGAAG CGCCTGCCTC 2400
245 CCCACTGCTC TGCCCCACCC TCCAATCTGC ACTTTGATTT GCTTCCTAAC AGCTCTGTTC 2460
247 CCTCCTGCTT TGGTTTTAAT AAATATTTTG ATGACGTAA AAAAAGGAAT TCGATAT 2517

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249 (2) INFORMATION FOR SEQ ID NO: 3:

251 (i) SEQUENCE CHARACTERISTICS:

252 (A) LENGTH: 2994 base pairs

253 (B) TYPE: nucleic acid

254 (C) STRANDEDNESS: single

255 (D) TOPOLOGY: linear

257 (ii) MOLECULE TYPE: cDNA

262 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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264 TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTGTAA CGGGAGTCGG GAGAGGACGG 60
266 GGCCTGCCCC GCGTGC GCGC GCGTCGTCTT CCCC GGCGCT CCTCCACAGC TCGCTGGCTC 120
268 CCGCCGCGGA AAGGCGTCAT GCCGCCCCAA ACCCCCCGAA AAACGGCCGC CACCGCCGCC 180
270 GCTGCCGCCG CGGAACCCCC GGCACCGCCG CCGCCGCCCT CTCCTGAGGA GGACCCAGAG 240
272 CAGGACAGCG GCCCGGAGGA CCTGCCTCTC GTCAGGCTTG AGTTTGAAGA AACAGAAGAA 300
274 CCTGATTTTA CTGCATTATG TCAGAAATTA AAGATACCAG ATCATGTCAG AGAGAGAGCT 360
276 TGGTTAACTT GGGAGAAAGT TTCATCTGTG GATGGAGTAT TGGGAGGTTA TATTCAAAG 420
278 AAAAAGGAAC TGTGGGGAAT CTGTATCTTT ATTGCAGCAG TTGACCTAGA TGAGATGTCTG 480
280 TTCACTTTTA CTGAGCTACA GAAAAACATA GAAATCAGTG TCCATAAATT CTTTAACTTA 540
282 CTAAGAGAAA TTGATACCAG TACCAAAGTT GATAATGCTA TGTCAGACT GTTGAAGAAG 600
284 TATGATGTAT TGTTTGCACT CTTAGCAAAA TTGGAAAGGA CATGTGAAGT TATATATTTG 660
286 ACACAACCCA GCAGTTCGAT ATCTACTGAA ATAAATTCTG CATTGGTGCT AAAAGTTTCT 720
288 TGGATCACAT TTTTATTAGC TAAAGGGGAA GTATTACAAA TGGAAGATGA TCTGGTGATT 780
290 TCATTTTCAGT TAATGCTATG TGTCTTGAC TATTTTATTA AACTCTCACC TCCCATGTTG 840
292 CTCAAAGAAC CATATAAAAC AGCTGTTATA CCCATTAATG GTTCACCTCG AACACCCAGG 900
294 CGAGGTCAGA ACAGGAGTGC ACGGATAGCA AAACAAC TAG AAAATGATAC AAGAATTATT 960
296 GAAGTTCTCT GTAAAGAACA TGAATGTAAT ATAGATGAGG TGAAAAATGT TTATTTCAAA 1020
298 AATTTTATAC CTTTATGAA TTCTCTTGGA CTTGTAACAT CTAATGGACT TCCAGAGGTT 1080
300 GAAAATCTTT CTAAACGATA CGAAGAAATT TATCTTAAAA ATAAAGATCT AGATGCAAGA 1140
302 TTATTTTGG ATCATGATAA AACTCTTCAG ACTGATTCTA TAGACAGTTT TGAAACACAG 1200
304 AGAACACCAC GAAAAAGTAA CCTTGATGAA GAGGTGAATG TAATTCCTCC ACACACTCCA 1260
306 GTTAGGACTG TTATGAACAC TATCCAACAA TTAATGATGA TTTTAAATTC AGCAAGTGAT 1320
308 CAACCTTCAG AAAATCTGAT TTCCTATTTT AACAACTGCA CAGTGAATCC AAAAGAAAGT 1380
310 ATACTGAAAA GAGTGAAGGA TATAGGATAC ATCTTTAAAG AGAAATTTGC TAAAGCTGTG 1440
312 GGACAGGGTT GTGTCGAAAT TGGATCACAG CGATACAAAC TTGGAGTTCT CTTGTATTAC 1500
314 CGAGTAATGG AATCCATGCT TAAATCAGAA GAAGAACGAT TATCCATTCA AAATTTTATG 1560
316 AAATCTCTGA ATGACAACAT TTTTCATATG TCTTTATTGG CGTGCCTCTT TGAGGTGTA 1620
318 ATGGCCACAT ATAGCAGAAG TACATCTCAG AATCTTGATT CTGGAACAGA TTTGTCTTTC 1680
320 CCATGGATTC TGAATGTGCT TAATTTAAAA GCCTTTGATT TTTACAAAGT GATCGAAAAGT 1740
322 TTTATCAAAG CAGAAGGCAA CTTGACAAGA GAAATGATAA AACATTTAGA ACGATGTGAA 1800
324 CATCGAATCA TGGAATCCCT TGCATGGCTC TCAGATTCAC CTTTATTTGA TCTTATTA 1860
326 CAATCAAAGG ACCGAGAAGG ACCAACTGAT CACCTTGAAT CTGCTTGTC TCTTAATCTT 1920
328 CCTCTCCAGA ATAATCACAC TGCAGCAGAT ATGTATCTTT CTCTGTAAAG ATCTCCAAAG 1980

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330 AAAAAAGGTT CAACTACGCG TGTAATTCT ACTGCAAATG CAGAGACACA AGCAACCTCA 2040
332 GCCTTCCAGA CCCAGAAGCC ATTGAAATCT ACCTCTCTTT CACTGTTTTA TAAAAAAGTG 2100
334 TATCGGCTAG CCTATCTCCG GCTAAATACA CTTTGTGAAC GCCTTCTGTC TGAGCACCCA 2160
336 GAATTAGAAC ATATCATCTG GACCCTTTTC CAGCACACCC TGCAGAATGA GTATGAACTC 2220
338 ATGAGAGACA GGCATTGGA CCAAATTATG ATGTGTTCCA TGTATGGCAT ATGCAAAGTG 2280
340 AAGAATATAG ACCTTAAATT CAAAATCATT GTAACAGCAT ACAAGGATCT TCCTCATGCT 2340
342 GTTCAGGAGA CATTCAAACG TGTTTTGATC AAAGAAGAGG AGTATGATTC TATTATAGTA 2400
344 TTCTATAACT CGGTCTTCAT GCAGAGACTG AAAACAAATA TTTTGCAGTA TGCTTCCACC 2460
346 AGGCCCCCTA CCTTGTCACC AATACCTCAC ATTCTCGAA GCCCTTACAA GTTTCCTAGT 2520
348 TCACCCCTTAC GGATTCCTGG AGGGAACATC TATATTTTAC CCCTGAAGAG TCCATATAAA 2580
350 ATTTTCAGAAG GTCTGCCAAC ACCAACAAAA ATGACTCCAA GATCAAGAAT CTTAGTATCA 2640
352 ATTGGTGAAT CATTCGGGAC TTCTGAGAAG TTCCAGAAAA TAAATCAGAT GGTATGTAAC 2700
354 AGCGACCGTG TGCTCAAAAG AAGTGCTGAA GGAAGCAACC CTCCTAAACC ACTGAAAAAA 2760
356 CTACGCTTTG ATATTGAAGG ATCAGATGAA GCAGATGGAA GTAAACATCT CCCAGGAGAG 2820
358 TCCAAATTTT AGCAGAAACT GGCAGAAATG ACTTCTACTC GAACACGAAT GCAAAAGCAG 2880
360 AAAATGAATG ATAGCATGGA TACCTCAAAC AAGGAAGAGA AATGAGGATC TCAGGACCTT 2940
362 GGTGGACACT GTGTACACCT CTGGATTCAT TGTCTCTCAC AGATGTGACT GTAT 2994

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364 (2) INFORMATION FOR SEQ ID NO: 4:

366 (i) SEQUENCE CHARACTERISTICS:

367 (A) LENGTH: 928 amino acids

368 (B) TYPE: amino acid

369 (C) STRANDEDNESS: Not Relevant

W--> 370 (D) TOPOLOGY: Not Relevant

372 (ii) MOLECULE TYPE: peptide

377 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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379 Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Thr Ala Ala Ala Ala
380 1 5 10 15
382 Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu Glu Asp
383 20 25 30
385 Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu
386 35 40 45
388 Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu
389 50 55 60
391 Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
392 65 70 75 80
394 Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys
395 85 90 95
397 Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu
398 100 105 110
400 Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val
401 115 120 125
403 His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val
404 130 135 140
406 Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
407 145 150 155 160
409 Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln
410 165 170 175
412 Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
413 180 185 190

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09315116.raw

Output Set: N:\CRF3\07172002\I315116.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:58 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=1
L:370 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=4
L:631 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:635 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:651 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:655 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:659 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:663 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:667 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:671 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:675 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:679 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:683 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:695 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:1079 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1083 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1099 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1127 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
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L:1537 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:33
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L:1565 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:33
L:1569 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:33
L:1573 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:33
L:1577 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:33
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L:1589 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:33
L:1613 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:33